

P1009PC00

1

SEQUENCE LISTING

<110> M&E Biotech A/S

<120> Novel Method For Down-Regulation Of Amyloid

<130> P1009PC1

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<160> 16

<170> PatentIn Ver. 3.0

<210> 1

<211> 2313

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(2313)

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<221> misc\_feature

<222> (2098)..(2169)

<223> nucleotides encoding transmembrane region

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<222> (2014)..(2313)

<223> Nucleotides encoding C-100

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<222> (2016)..(2144)

<223> Abeta 42/43

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&lt;222&gt; (2014)..(2142)

&lt;223&gt; Abeta 42/43

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 Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg  
 1 5 10 15

gcg ctg gag gta ccc act gat ggt aat gct ggc ctg ctg gct gaa ccc 96  
 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
 20 25 30

cag att gcc atg ttc tgt ggc aga ctg aac atg cac atg aat gtc cag 144  
 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
 35 40 45

aat ggg aag tgg gat tca gat cca tca ggg acc aaa acc tgc att gat 192  
 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
 50 55 60

acc aag gaa ggc atc ctg cag tat tgc caa gaa gtc tac cct gaa ctg 240  
 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
 65 70 75 80

cag atc acc aat gtg gta gaa gcc aac caa cca gtg acc atc cag aac 288  
 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
 85 90 95

tgg tgc aag cgg ggc cgc aag cag tgc aag acc cat ccc cac ttt gtg 336  
 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
 100 105 110

att ccc tac cgc tgc tta gtt ggt gag ttt gta agt gat gcc ctt ctc 384  
 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
 115 120 125

gtt cct gac aag tgc aaa ttc tta cac cag gag agg atg gat gtt tgc 432  
 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys  
 130 135 140

gaa act cat ctt cac tgg cac acc gtc gcc aaa gag aca tgc agt gag 480  
 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
 145 150 155 160

aag agt acc aac ttg cat gac tac ggc atg ttg ctg ccc tgc gga att 528  
 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
 165 170 175

gac aag ttc cga ggg gta gag ttt gtg tgt tgc cca ctg gct gaa gaa 576  
 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
 180 185 190

agt gac aat gtg gat tct gct gat gcg gag gag gat gac tgc gat gtc 624  
 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
 195 200 205

tgg tgg ggc gga gca gac aca gac tat gca gat ggg agt gaa gac aaa 672  
 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
 210 215 220

gta gta gaa gta gca gag gag gaa gaa gtg gct gag gtg gaa gaa gaa 720  
 Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
 225 230 235 240

gaa gcc gat gat gac gag gac gat gag gat ggt gat gag gta gag gaa 768  
 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
 245 250 255

gag gct gag gaa ccc tac gaa gaa gcc aca gag aga acc acc agc att 816  
 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
 260 265 270

gcc acc acc acc acc acc acc aca gag tct gtg gaa gag gtg gtt cga 864  
 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
 275 280 285

gag gtg tgc tct gaa caa gcc gag acg ggg ccg tgc cga gca atg atc 912  
 Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
 290 295 300

tcc cgc tgg tac ttt gat gtg act gaa ggg aag tgt gcc cca ttc ttt 960  
 Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
 305 310 315 320

tac ggc gga tgt ggc ggc aac cgg aac aac ttt gac aca gaa gag tac 1008  
 Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
 325 330 335

tgc atg gcc gtg tgt ggc agc gcc atg tcc caa agt tta ctc aag act 1056  
 Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr  
 340 345 350

acc cag gaa cct ctt gcc cga gat cct gtt aaa ctt cct aca aca gca 1104  
 Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala  
 355 360 365

gcc agt acc cct gat gcc gtt gac aag tat ctc gag aca cct ggg gat 1152  
 Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp  
 370 375 380

gag aat gaa cat gcc cat ttc cag aaa gcc aaa gag agg ctt gag gcc 1200  
 Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala  
 385 390 395 400

aag cac cga gag aga atg tcc cag gtc atg aga gaa tgg gaa gag gca 1248  
 Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala  
 405 410 415

gaa cgt caa gca aag aac ttg cct aaa gct gat aag aag gca gtt atc 1296  
 Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile  
 420 425 430

cag cat ttc cag gag aaa gtg gaa tct ttg gaa cag gaa gca gcc aac 1344  
 Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn  
 435 440 445

gag aga cag cag ctg gtg gag aca cac atg gcc aga gtg gaa gcc atg 1392  
 Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met  
 450 455 460

[illegible]

4

cag gct gtt cct cct cgg cct cgt cac gtg ttc aat atg cta aag aag 1488  
Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys  
485 490 495

gag cat gtg cgc atg gtg gat ccc aag aaa gcc gct cag atc cgg tcc 1584  
Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser  
515 520 525

cag gtt atg aca cac ctc cgt gtg att tat gag cgc atg aat cag tct 1632  
Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser  
530 535 540

ctc tcc ctg ctc tac aac gtg cct gca gtg gcc gag gag att cag gat 1680  
Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp  
545 550 555 560

gaa gtt gat gag ctg ctt cag aaa gag caa aac tat tca gat gac gtc 1728  
Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val  
565 570 575

ttg gcc aac atg att agt gaa cca agg atc agt tac gga aac gat gct 1776  
Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala  
580 585 590

ctc atg cca tct ttg acc gaa acg aaa acc acc gtg gag ctc ctt ccc 1824  
Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro  
595 600 605

gtg aat gga gag ttc agc ctg gac gat ctc cag ccg tgg cat tct ttt 1872  
Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe  
610 615 620

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ggg gct gac tct gtg cca gcc aac aca gaa aac gaa gtt gag cct gtt 1920
Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625                630                635                640

gat gcc cgc cct gct gcc gac cga gga ctg acc act cga cca ggt tct 1968
Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
        645                650                655

ggg ttg aca aat atc aag acg gag gag atc tct gaa gtg aag atg gat 2016
Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
        660                665                670

gca gaa ttc cga cat gac tca gga tat gaa gtt cat cat caa aaa ttg 2064
Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
        675                680                685

gtg ttc ttt gca gaa gat gtg ggt tca aac aaa ggt gca atc att gga 2112
Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
        690                695                700

ctc atg gtg ggc ggt gtt gtc ata gcg aca gtg atc gtc atc acc ttg 2160
Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705                710                715                720

gtg atg ctg aag aag aaa cag tac aca tcc att cat cat ggt gtg gtg 2208
Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
        725                730                735

gag gtt gac gcc gct gtc acc cca gag gag cgc cac ctg tcc aag atg 2256
Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
        740                745                750

cag cag aac ggc tac gaa aat cca acc tac aag ttc ttt gag cag atg 2304
Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
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cag aac tag 2313
Gln Asn
770

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<211> 770

<212> PRT

<213> Homo sapiens

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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro

20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln

35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp

50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu

65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn

85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val

100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu

115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys

130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu

145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile

165 170 175

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8

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
290 295 300

Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr  
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala  
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp  
370 375 380



Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala  
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala  
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile  
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn  
435 440 445

Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met  
450 455 460

Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu  
465 470 475 480

Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys  
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe  
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser  
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser  
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp  
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val  
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala  
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro  
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe  
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val  
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser  
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp  
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu  
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly  
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu  
705 710 715 720

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val  
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met  
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met  
755 760 765

Gln Asn  
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<210> 3

<211> 45

<212> DNA

<213> Clostridium tetani

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&lt;221&gt; CDS

&lt;222&gt; (1)..(45)

&lt;223&gt; DNA encoding P2 epitope

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cag tac atc aaa gct aac tcc aaa ttc atc ggt atc acc gag ctg 45

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu

1

5

10

15

&lt;210&gt; 4

&lt;211&gt; 15

&lt;212&gt; PRT

&lt;213&gt; Clostridium tetani

&lt;400&gt; 4

Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu

1

5

10

15

&lt;210&gt; 5

&lt;211&gt; 63

&lt;212&gt; DNA

&lt;213&gt; Clostridium tetani

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(63)

&lt;223&gt; DNA encoding P30 epitope

&lt;400&gt; 5

ttc aac aac ttc acc gta agc ttc tgg ctg cgt gtt ccg aaa gtt agc 48

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser

1

5

10

15

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12

gct agc cac ctg gaa  
Ala Ser His Leu Glu  
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63

<210> 6

<211> 21

<212> PRT

<213> Clostridium tetani

<400> 6

Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys Val Ser  
1 5 10 15

Ala Ser His Leu Glu  
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<210> 7

<211> 21

<212> DNA

<213> Synthetic

<400> 7

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21

<210> 8

<211> 21

<212> DNA

<213> Synthetic

<400> 8

agatctcgat cccgcgaaat t

21

<210> 9

<211> 135

<212> DNA

<213> Synthetic

<400> 9

atggatgcag aattccgtca cgactccggt tacgaagttc accaccagaa actgggttttc

60

13

ttcgcagaag atgttgggtc caacaaagggt gcaatcatcg gtctgatggt tggcgggtgtt 120  
gttatcgcga cctag 135

&lt;210&gt; 10

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Synthetic

&lt;400&gt; 10

gccggccatg gatgcagaat tccgtcacga c 31

&lt;210&gt; 11

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Synthetic

&lt;400&gt; 11

gccggaagct tctaggtcgc gataacaaca ccgccaacc 39

&lt;210&gt; 12

&lt;211&gt; 84

&lt;212&gt; DNA

&lt;213&gt; Synthetic

&lt;400&gt; 12

ccggcaagct tctacagctc ggtgataccg atgaatttgg agttagcttt gatgtactgg 60  
gtcgcgataa caacaccgcc aacc 84

&lt;210&gt; 13

&lt;211&gt; 101

&lt;212&gt; DNA

&lt;213&gt; Synthetic

&lt;400&gt; 13

gccggccatg ggtttcaaca acttcaccgt tagcttctgg ctgcgtgttc cgaaagttag 60  
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&lt;210&gt; 14

&lt;211&gt; 172

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<212> DNA

<213> Synthetic

<400> 14

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ccggagtcgt gacggaactc tgcattccagc tcggtgatac cgatgaattt gg          172
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<210> 15

<211> 30

<212> DNA

<213> Synthetic

<400> 15

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<210> 16

<211> 35

<212> DNA

<213> Synthetic

<400> 16

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